

卷之三

FHF-1	-----MAAAIASSLIRQKROARESNS-DRVSASKRRSSPSKDG-R	38
FGF-10	-----MAAAIASGLIRQKRQAREQHW-DRPSASRRRSPSKN--R	37
FHF-4	-----MAAAIASSLIRQKRQARER--EKSACKCVSSPSKG--K	35
FHF-2	-----MAALASSLIRQKREVREPGG-SRPVSAQRVRCP-RGT-K	36
FHF-3	-----MS-GPGTAAVALLPAVLLALL-APWAGRGGAAAPTAPN-G	37
FGF4 HUMAN	MALGQQLFITMSRGAGRLQGTLWALVFLGIL-VGMVVP--SPAGTRAN-N	46
FGF6 HUMAN	-----	
FGF2 HUMAN	-----	
FGF1 HUMAN	-----	
KGF-2	-----MWKWLTHCASAFPHLPGCCC-CCFLLLFLVSSVPVTC-Q	38
FGF7 HUMAN	-----MHKWILTWLPTLLYR-S-----CFHIICLVGTISLAC-N	33
ZGI HUZFGF	-----MY-SAPSACTCLCLHFLLCF-QVQ-----VLVAEE-N	30
FGF8 HUMAN	-----MG-SPRSALSCLLLHLLVLCL-QAQEGPGRGPALGRE-A	37
FGF5 HUMAN	-----MSLSFLLLLFFSHLILSAWAHGEKRLAPKGOPGPAATDRN	40
FGF9 HUMAN	-----MAPLGEVGNYFGVQDAVPFGNPVLP--VDSPVLLS-D	35
FGF3 HUMAN	-----MGLIWLLLLSLEP-----G-----WPAAGPGA	23

FHF-1	SLCERHV---LGVFSKVRFCSGR-----KRPVRRRPEPKLGIVT	75
FGF-10	-----MASKEPQLKGIVT	13
FHF-4	GLCNGNL---VDIFSKVRIFGLK-----KRRRLRQ-DPQLKGIVT	73
FHF-2	TSCDKNK---LNVFSRVKLFGSK-----KRRRRRP-EPQLKGIVT	71
FHF-3	SLCQKQL---LILLSKVRLCGGRP-----ARPDRGP-EPQLKGIVT	73
FGF4 HUMAN	TLEAELEERR-WESLVALSLARLPVAAQPK-AAVQSGAGDYLLG-IKRLR	84
FGF6 HUMAN	TLLDS--RG-WGTLLSRSRAGL--AG--E-IAGVNWESGYLVG-IKRQR	86
FGF2 HUMAN	-----MAAGSITTLPALPE-----DGGSGAFPPGHFKDPK	30
FGF1 HUMAN	-----MAEGETTTFTALTE-----KFN--LPPGNYKKPK	27
KGF-2	ALGQDMVSP-EATNSSSSFSSPSSAG-----RHVRSYNHLOQ-DVRWR	80
FGF7 HUMAN	DMTPEQM---ATVNCS--SPE-----RHTRSYDYMEEGDIRVR	67
ZGI HUZFGF	VDFRHI---VEN-----QTRARDDVSRKQLRLY	55
FGF8 HUMAN	SLFRAGR---EPOGVSQHQHRE-----QSLVTDQLSRRRLIRTY	72
FGF5 HUMAN	PIGSSSRQSSSAMSSSSASSSPAASLGSQGSGLEQSSFQWSPS-GRTG	89
FGF9 HUMAN	HLGQS-----E--AGGLPRGP-----AVTDLDHLKG-ILRRR	64
FGF3 HUMAN	RLRRD-----AGG-----RGGVYEHLLG-APRRR	46

FHF-1	RLFSQQ--GYFLQMHPDGTIDGTDENSDYTLFNLIPVGLR-VVAIQVK	122
FGF-10	RLFSQQ--GYFLQMHPDGTIDGTDENSDYTLFNLIPVGLR-VVAIQVK	60
FHF-4	RLYCRQ--GYYLQMHPDGAIDGKDSTNSTLFNLIPVGLR-VVAIQVK	120
FHF-2	KLYSRQ--GYHLQLQADGTIDGTDENSDYTLFNLIPVGLR-VVAIQVK	118
FHF-3	KLFCRQ--GFYLNQANPDGSIOGTPEDTSSFTHFNLIPVGLR-VVTIQS	120
FGF4 HUMAN	RLYCNVGIGFHLQALPDGRIGGAAHDT-RDSLLELSPVERG-VVSIFGVA	132
FGF6 HUMAN	RLYCNVGIGFHLQVLPDGRISGTHEEN-PYSLLEISTVERG-VVSLFGVR	134
FGF2 HUMAN	RLYCKNG-GFFLRIPHDPGRVDGVREKSDPHIKLQLQAEERG-VVSIKGVC	78
FGF1 HUMAN	LLYCSNG-GHFLRILPDGTVGDGTRDRSDQHQLQLSAESVG-EVYIKSTE	75
KGF-2	KLFSFT--KYFLKIEKNGKVSGTKKENCPYSILEITSVEIG-VVAVKAIN	127
FGF7 HUMAN	RLFCRT--QWYLRIDKRGKVGTQEMKNNNIMEIRTVAVG-IVAIKGVE	114
ZGI HUZFGF	QLYSRTS-GKHIQVLG-RRISARGEDGDKYAQLLVETDTFGSQVRIGKE	103
FGF8 HUMAN	QLYSRTS-GKHVQVLANKRINAMAEDGDPFAKLIVETDTFGSRVVRGAE	121
FGF5 HUMAN	SLYCRVGIGFHLQIYPDGVNGSHEAN-MLSVLEIFAVSQG-IVGIRGVF	137
FGF9 HUMAN	QLYCRT--GFHLEIFPNGTIQGTRKDHSRGILEFISIAVG-LVSIRGV	111
FGF3 HUMAN	KLYCAT--KYHLQLHPSGRVNGSLENS-AYSILEITAVEVG-IVAIRGLF	92

Fig. 1

JOURNAL OF CLINICAL ONCOLOGY

FHF-1	ASLYVAMNGEGLYSSDV-FTPECKFKEVFENYYVIYSSTLYRQQESG-	170
FGF-10	ASLYVAMNGEGLYSSDV-FTPECKFKEVFENYYVIYSSTLYRQQESG-	108
FHF-4	TGLYIAMNGEGLYLYPSEL-FTPECKFKEVFENYYVISSMLYRQQESG-	168
FHF-2	TKLYLAMNSEGYLYTSEL-FTPECKFKEVFENYYVTYSSMIYRQQSG-	166
FHF-3	LGHYMAMNAEGLLYSSPH-FTAECRFKECVFENYYLYASALYRQRSG-	168
FGF4_HUMAN	SRFFVAMSSKGKLYGSPF-FTDECTFKEILLPNNNAYESYKPG-----	176
FGF6_HUMAN	SALFVAMNSKGRLYATPS-FQEECKFRETLLPNNNAYESDLYOG-----	178
FGF2_HUMAN	ANRYLAMKEDGRLLASKC-VTDECFFFERLESNNYNTYRSRKYTS-----	122
FGF1_HUMAN	TGQYLAMTDGLLYGSQT-PNEECLFLERLEHYNTYISKHAEK--N-	121
KGF-2	SNYYLAMNKKGKLYGSKE-FNNNDCKLKERIEENGNTYASFNWQHN--G-	173
FGF7_HUMAN	SEFYLAMNKEGKLYAKKE-CNEDCNFKELILEHYNTYASAKWTHN--G-	160
ZGI_HUZFGF	TEFYLCMNRKGKLVGKPDGTSKECVFIEKVLENNYTALMSAKYSG-----	148
FGF8_HUMAN	TGLYICMNKKGKLIAKSNGKGKDCVFTIEVLENNYTALQNAKYEG-----	166
FGF5_HUMAN	SNKFLAMSKKGKLHASAK-FTDDCKFRERFQENSNTYASAIHRTEKTG-	185
FGF9_HUMAN	SGLYLGMEKGELYGSEK-LTQECVFREQFEENWYNTYSSNLYKHDTG-	159
FGF3_HUMAN	SGRYLAMNKRGRLYASEH-YSAECEFVERIHELGYNTYASRLYRTVSSTP	141
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FHF-1	-----RAWFLGLNKEGQIMKG--NRVKKTPSSHFPKPPIEVCMYR	209
FGF-10	-----RAWFLGLNKEGQIMKG--NRVEKTPSSHFPKPPIEVCMYR	147
FHF-4	-----RAWFLGLNKEGQAMKG--NRVKKTPAAHFLPKPLEVAMYR	207
FHF-2	-----RGWYLGLNKEGEIMKG--NHVKKNPAAHFLPKPLKVAMYK	205
FHF-3	-----RAWYLGLDKEGQVMKG--NRVKKTKAAAHFLPKLLEVAMYQ	207
FGF4_HUMAN	-----MFIALSKNGKTKKG--NRVSPPTMKVTHFLPRL-----	206
FGF6_HUMAN	-----TYIALSKYGRVKG--SKVSPIMTVTHFLPRI-----	208
FGF2_HUMAN	-----WYVALKRTGQYKLG--SKTGPQKAILFLPLMSAKS-----	155
FGF1_HUMAN	-----WFVGLKKNGSCKRG--PRTHYQKAILFLPLPVSSD-----	155
KGF-2	-----RQMYVALNGKGAPRRG--QKTRRKNTSAHFLPMVVHS-----	208
FGF7_HUMAN	-----GEMFVALNQKGIPVRG--KKTKEQKTAHFLPMAIT-----	194
ZGI_HUZFGF	-----WYVGFTKKGRPRKG--PKTRENQQDVHFMKRYPKGQPEL	185
FGF8_HUMAN	-----WYMAFRKGRPRKG--SKTRQHQREVFHMKRLPRGHHTT	203
FGF5_HUMAN	-----REWYVALNKRGKAKGCSPRVKPQHISTHFLPRFKQSEQ-P	225
FGF9_HUMAN	-----RYYVALNKDGTPREG--TRTKRHQKFTHFLPRPVDPDKVP	198
FGF3_HUMAN	GARRQPSAERLWYVSVNGKGPRRRG--FKTRRTQKSSLFLPRVLDHRDHE	189
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FHF-1	EPSLHEIGEKQ---GRS--RKSSGTPTMNGGKVNVQDST-----	243
FGF-10	EPSLHEIGENK---GVQ--GKFWTPP-----	168
FHF-4	EPSLHDVGETVPKP-GVTPSKSTSASAIMNGGKPVNKSHT-----	247
FHF-2	EPSLHDLTEFSRSG-SGTPTKSRVSGVLNGGKSMHNEST-----	245
FHF-3	EPSLHSVPEAS-----P--SSPPAP-----	225
FGF4_HUMAN	-----	
FGF6_HUMAN	-----	
FGF2_HUMAN	-----	
FGF1_HUMAN	-----	
KGF-2	-----	
FGF7_HUMAN	-----	
ZGI_HUZFGF	QKPFKYTTVK--RSRR--IRPTHFA-----	207
FGF8_HUMAN	EQSLRFEFLNYPPF-TRSLRGSQRTWAPEPR-----	233
FGF5_HUMAN	ELSFTVTVEKKNP-PSPISKIPLSAPRKNTNSVKYRLKFRFG-----	268
FGF9_HUMAN	ELYKDILSQS-----	208
FGF3_HUMAN	MVRQLQSGLPRPPGKGVQPRRRRQKQSPDNLEPSHVQASRLGSQLEASAH	239

Fig. 2

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	1.00	0.39	0.43	0.29	0.46	0.33	0.36	0.38	0.37	0.41	0.39	0.40	0.42	0.40	0.35	0.38
2		1.00	0.38	0.34	0.41	0.35	0.38	0.33	0.38	0.44	0.39	0.37	0.37	0.39	0.35	0.60
3			1.00	0.31	0.42	0.34	0.33	0.36	0.34	0.38	0.35	0.37	0.41	0.46	0.35	0.35
4				1.00	0.34	0.53	0.26	0.24	0.26	0.31	0.28	0.30	0.30	0.30	0.31	0.28
5					1.00	0.35	0.39	0.43	0.39	0.39	0.43	0.42	0.44	0.44	0.43	0.43
6						1.00	0.33	0.31	0.33	0.31	0.32	0.34	0.34	0.32	0.36	0.36
7							1.00	0.34	0.98	0.33	0.76	0.81	0.34	0.37	0.67	0.42
8								1.00	0.34	0.54	0.34	0.37	0.36	0.36	0.34	0.38
9									1.00	0.33	0.66	0.72	0.34	0.37	0.62	0.42
10										1.00	0.32	0.35	0.40	0.37	0.32	0.43
11											1.00	0.68	0.36	0.38	0.58	0.41
12												1.00	0.36	0.33	0.62	0.42
13													1.00	0.47	0.34	0.32
14														1.00	0.30	0.31
15															1.00	0.38
16																1.00

Fig. 3

10 20 30 40 50 60
HZFGF5 EENVDFRIHVENQTRARDDVSRKQLRLYQLYSRTSGKHIQVLGRRISARGEDGDKYAQLL
::: :::::::::::::::::::::
MZFGF5 EENVDFRIHVENQTRARDDVSRKQLRLYQLYSRTSGKHIQVLGRRISARGEDGDKYAQLL

10 20 30 40 50 60
70 80 90 100 110 120
HZFGF5 VETDTFGSQVRIGKETEFYLCMNRKGKLVGKPDGTSKECVFIEKVLENNYTALMSAKYS
::: :::::::::::::::::::::
MZFGF5 VETDTFGSQVRIGKETEFYLCMNRKGKLVGKPDGTSKECVFIEKVLENNYTALMSAKYS
70 80 90 100 110 120
130 140 150 160 170 180
HZFGF5 GWYVGFTKKGRPRKGPKTRENQQDVHFMKRYPKGQPELQKPFKYTTVTRSRRIRPTHPA
::: :::::::::::::::::::::
MZFGF5 GWYVGFTKKGRPRKGPKTRENQQDVHFMKRYPKGQAELOKPFKYTTVTRSRRIRPTHPG
130 140 150 160 170 180

Fig. 4